STIC Biotechnology Systems Branch

CRF Problem Report

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: _10/593,426_
Filing Date: _9/19/06_
Date Processed by STIC: _9/27/06_

STIC Contact: **Mark Spencer: Telephone: 571-272-2510; Fax: 571-273-0221**

Nature of CRF Problem:

____ (circle one) Damaged or Unreadable (for Unreadable, see attached)
____ Blank (no files on CRF) (see attached)
____ Empty file (filename present, but no bytes in file) (see attached)
____ Wrong file saved to CRF (invention title, docket number, or applicant(s) do not match those in official application)   (see attached)
____ Not saved in ASCII text
____ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should **only** be the Sequence Listing.
____ Did not contain a Sequence Listing. (see attached sample)
_✓_ Other: _Alpha Numeric headings in Sequence._

PLEASE USE THE CHECKER VERSION 4.3.1 PROGRAM TO REDUCE ERRORS.
SEE BELOW FOR ADDRESS:
        http:/www.uspto.gov/web/offices/pac/checker/chkrnote.htm

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission User Manual - ePAVE**)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 08/30/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER _10/593,426_

ATTN; NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓ Wrapped Nucleics — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
  Wrapped Aminos — was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
  prevent "wrapping."

2 _____ Invalid Line Length — The rules require that a line **not exceed 72** characters in length. This includes white spaces.

3 _____ Misaligned Amino — The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
  Numbering — use **space characters**, instead.

4 _____ Non-ASCII — The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
  ensure your subsequent submission is saved in ASCII text.**

5 _____ Variable Length — Sequence(s)_____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
  each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
  residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
  "bug" — sequences(s) _____. Normally, PatentIn would automatically generate this section from the
  previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
  the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
  Artificial or Unknown sequences.**

7 _____ Skipped Sequences — Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
  (OLD RULES) — (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
  (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
  This sequence is intentionally skipped

  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 _____ Skipped Sequences — Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
  (NEW RULES) — <210> sequence id number
  <400> sequence id number
  000

9 _____ Use of n's or Xaa's — Use of n's and/or Xaa's have been detected in the Sequence Listing.
  (NEW RULES) — Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
  In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10 ✓ Invalid <213> — Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
  Response — scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
  is Artificial Sequence

11 _____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
  "Unknown." Please explain source of genetic material in <220> to <223> section.
  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
  "bug" — resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
  listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa — "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

SEQUENCE LISTING
<110> PAPES, Fabio
    GERHARDT, Isabel Rodrigues
    ARRUDA, Paulo

<120> CAMBIUM/XYLEM-PREFERRED PROMOTERS AND USES THEREOF

<130> ALEL 202.1 PCT

<140> *pls insert prior Application Number and date,*
<141>

<150> US 60/560,227
<151> 2004-04-06

<160> 41

<170> PatentIn version 3.2

pls delete, invalid numeric identifier.

These types of errors are seen globally throughout the sequence.

<200> SEQUENCE CHARACTERISTICS:
<210> SEQ ID NO 1
<211> LENGTH: 3035
<212> TYPE: DNA
<213> ORGANISM: Populus sp.
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)...(3035)
<223> OTHER INFORMATION: Sucrose synthase (SUSY) promoter
<400> SEQUENCE: 1

pls delete

pls do NOT insert Alpha numeric headings in sequence,

tcatgtccta tccaacggcg atgcaaactt cgctgtcccg cacttttttca taggacgagg tgaagtttag   70
ctatatatct tttttttta atttaaattg ttaattcttt atattttat attcttttaa ttttatattt
140
ttatattatt ttgatatatt acatcaagaa taaatttaa aaaaataatt tttaaaattt acttaaccac
210
gcaatacata aaaaataata gaacccacca acctaagaat acttgtcaat gcatagaagt acacctgcta
280
gttcttaaaa ccaacaaaag gaagcaaagt agatctctga gtcaaaaacc agaggaaacc atagaaacac
350
ataataataa taataataat aataataata aaattaattt aacttggtgt aataataaaa ttaatttaat
420
tacaaagagt gtaactcaac tagtcatgtt ctaaatttat tctctagaga ttactagttt gagttttaca
490
aattttaagg ccactgaaga tttatatagt cattaatttc agaatatata agattagttg agttacgtat
560
aacttgatta aaaaatcata ttaataaaaa taaaaaaatt aatttaaagg tttaagaaat caaattaaga
630
gaaaagagtg gtgtttttatt tttcatcgtg ccctctctca acagacaagt agaatgatga gagagagagg
700
gtaaagaaat ggatttatga gaacattgac cacagggaaa gagagaagcg gttttgtgaa aggaacaatg
770
aaaccacagg aaggtaaagc ggtaatgata tatttcacga atactaaaac tagaacaaca agttttttaa
840
tcaaattaaa ccacgagtgc aaggccgtct tctctgtgta taaaagggtc cttcttcttt ctcatttccc
910
attctcatct gcaaacttct cctttgcaat ctttctttct tgcgttctgt gtgttcgttg tgatttgtgt
980

pls see item #1 on error Summary sheet.

```
tcattcttct tgtctattag cttgtccccc cgtccgactg ctttctgtat ttattctggc attaagctta
1050
aggtaaagat ccctcaacta tcccaagcaa tttattctgt ttttatgtga tcttgaggga tcttcctctt
1120
ggatgcgctt tttatttttt cttcctcctt cttcctgctc cttcttacct tgtatctgat cccccagacg
1190
aaaatgtttt ttgttttttt aattagctca acaaatcaaa aacattcaca taataacaca gctcgaaaga
1260
aatctgatac agttttaatc tgttgtattt taaaaatcat tacagttcat gcatgctgat actttaccat
1330
gtcatgaaat taaatcccag catccttttc catagccaaa gaaggatcag cagcatgctg atagtttacc
1400
atgtcatgaa attaaatccc agcatccttt tccatagcca agaaagatc agcagcatgc ttgcttatac
1470
aaggtcttcg cttgcttatc aaggccactg aaacatcatc atcgtcataa ctatgataga acccgcctac
1540
tgccggcatt gaaaacatca tcactagtgt ctctacatta aaaaacaccc actgtctaat ttcctatttt
1610
tttactctta aaatgtcttt cggcttgagc tcctcgggct ccacggatgg caactgctgt attatatata
1680
tatatatata tatatatata tatatatata tatatatata tatatatata tatatttccc tgttggctac
1750
atagacctgt taataccgta taaatagata atattaatat atagaattca tgtatctttc cgagattaag
1820
cgatgccgta taaataatat taatatcttt gaatcagtat gtatattaat taaaattaat tttttttcaaa
1890
gtaattttaa gagcgcattt tcaacatcca tttagttttt ttttaataat aaatctctct ttgcattaat
1960
cctaacgttt gaacttagta aattaaaaaa aggaaaatac cttttttcacc aatatagaat caatgaacag
2030
cactagtttg cttgaaataa aaataaaaat aaaatctaat aagacatttc gaaatcatcc ttatccgcaa
2100
atcactacat tagtatagta tcttgaaaga taagcaagga tcatgcaagt ttataataat taaacttaaa
2170
acgtactatg acgtgtgcat cattcattca ttctgcatga aactctccac aagtctagcc tttgcatcat
2240
tcattctact tcattttatt ttttcctcta atggtttcga ttgatttttc tttcttagag tctggtcttt
2310
tagttcaact ttacatgttt taggctcgta ttttgagaga aaaaaaagaa aaaagtatgc agatcatgat
2380
tctgcaaaat actgaactag tgttctgatg aattaacatg tagcatgtat aatgctggaa gaactaaaga
2450
gcagttgggc tgccatgacc aaaagaaact tcgactgatt ataaatgtca aaacttgggc ccattctttg
2520
gtttctgtct gttgttttat gccatggcaa aactctgctt atttttcaac gtccaacgtc aaatgggaga
2590
ggtttaaatt ctattgttat gtctaaacca cgtggttgtt atctatatct gaccgaacat tcaagctttt
2660
ggtattccac aagaagggtt ttctctcttc tttcttttca taattgtaat gtgtttaatt tgtttcttgc
2730
ccaataatct tctctgcttc aaactaactt taattgttcg atctcttgcg ttattttaga catgtgcaat
2800
cacctttcac tgttgaaaaa atggttggtg aggtgaggtg gtaggttttg aagtcttcta gaataatgtg
2870
gtttctctgt tgctcttgac ttcttcttgt agatcatttc tggctggcta agctatccat acccccccgc
2940
ccctacaaat aatattgagt tgttgctggt cttaattcct attatctgtt attactccca ctgattgctt
```

3010
tctgtttctc ttaaggagct atggc   ← Same
3035   error

10/593,426

```
<200>  SEQUENCE CHARACTERISTICS:
<210>  SEQ ID NO 13
<211>  LENGTH: 31
<212>  TYPE: DNA
<213>  ORGANISM/SOURCE: synthetic
<221>  NAME/KEY: primer/oligonucleotide
<400>  SEQUENCE: 13
5-  GCCATAGCTC CTTAAGAGAA ACAGAAAGCA A -3
```

pls delete, Invalid numeric identifier

Invalid response — insert on line <223>

delete

pls use lower case

delete

see item #10 on error summary sheet.

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

FYI:

<213> responses CAN ONLY be either Artificial/Unknown or genus/species,